

## Sequence Listing

<110> Botstein,David

Desnoyers,Luc

Ferrara,Napoleone

Fong,Sherman

Gao,Wei-Qiang

Goddard,Audrey

Gurney,Austin L.

Pan,James

Roy,Margaret Ann

Stewart,Timothy A.

Tumas,Daniel

Watanabe,Colin K.

Wood,William I.

<120> Secreted and Transmembrane Polypeptides and Nucleic  
Acids Encoding the Same

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Phe Ala Ile Ala Arg Arg Leu Ala Gln Asp Gly Ala His Val Val  
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Val Ser Ser Arg Lys Gln Gln Asn Val Asp Gln Ala Val Ala Thr  
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35 40 45  
Phe Val Pro Arg Pro His Thr Ala Pro Leu Gly Gly Ala His Ala  
50 55 60  
His Val Leu Gly Met Val Pro Pro Ala Cys Leu Pro Gly Asp Glu  
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Ala Gly Ala Glu Leu Leu Thr Glu Val Asn Arg Leu Gly Ser Gly  
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                   365                     370                 375  
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Ser Gln Ala Leu Asn Glu Asp Ile Val Arg Val Ser Ser Arg Leu 455	460	465
Glu His Leu Glu Lys Glu Leu Ser Glu Lys Ser Gly Gln Leu Arg 470	475	480
Gln Gly Ser Ala Gln Ser Gln Gln Ile Arg Gly Glu Ile Asp 485	490	495
Ser Leu Arg Gln Glu Lys Asp Ser Leu Leu Lys Gln Arg Leu Glu 500	505	510
Ile Asp Gly Lys Leu Arg Gln Gly Ser Leu Leu Ser Pro Glu Glu 515	520	525
Glu Arg Thr Leu Phe Gln Leu Asp Glu Ala Ile Glu Ala Leu Asp 530	535	540
Ala Ala Ile Glu Tyr Lys Asn Glu Ala Ile Thr Cys Arg Gln Arg 545	550	555
Val Leu Arg Ala Ser Ala Ser Leu Leu Ser Gln Cys Glu Met Asn 560	565	570
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Arg Gln Arg Leu Glu Met Asp Arg Gln Leu Thr Leu Gln Gln Lys 635	640	645
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His Leu Gly Glu Gly Leu Ala Asp Ser Arg Arg Gln Tyr Glu Ala 665	670	675
Arg Ile Gln Ala Leu Glu Lys Glu Leu Gly Arg Tyr Met Trp Ile 680	685	690

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725 730 735

Leu Trp Leu Ser Pro Leu Thr Glu Gly Ala Pro Arg Thr Arg Glu  
740 745 750

Glu Thr Arg Asp Leu Val His Ala Pro Leu Pro Leu Thr Trp Lys  
755 760 765

Arg Ser Ser Leu Cys Gly Glu Glu Gln Gly Ser Pro Glu Glu Leu  
770 775 780

Arg Gln Arg Glu Ala Ala Glu Pro Leu Val Gly Arg Val Leu Pro  
785 790 795

Val Gly Glu Ala Gly Leu Pro Trp Asn Phe Gly Pro Leu Ser Lys  
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Leu Ser Leu Lys Glu Thr Arg Arg Cys Gly Ser Thr Cys Thr Phe  
65 70 75  
Trp Pro Cys Phe Glu Leu Cys Cys Pro Glu Ser Phe Gly Pro Gln  
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Gln Lys Phe Leu Val Lys Leu Arg Val Leu Gly Met Lys Ser Gln  
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<213> Homo sapiens

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Ile Pro Leu Glu Lys Leu Ala Gln Ala Pro Glu Gln Pro Gly Gln  
35 40 45  
Glu Lys Arg Glu His Ala Thr Arg Asp Gly Pro Gly Arg Val Asn  
50 55 60  
Glu Leu Gly Arg Pro Ala Arg Asp Glu Gly Gly Ser Gly Arg Asp  
65 70 75  
Trp Lys Ser Lys Ser Gly Arg Gly Leu Ala Gly Arg Glu Pro Trp  
80 85 90  
Ser Lys Leu Lys Gln Ala Trp Val Ser Gln Gly Gly Ala Lys  
95 100 105  
Ala Gly Asp Leu Gln Val Arg Pro Arg Gly Asp Thr Pro Gln Ala  
110 115 120  
Glu Ala Leu Ala Ala Ala Gln Asp Ala Ile Gly Pro Glu Leu  
125 130 135  
Ala Pro Thr Pro Glu Pro Pro Glu Glu Tyr Val Tyr Pro Asp Tyr  
140 145 150  
Arg Gly Lys Gly Cys Val Asp Glu Ser Gly Phe Val Tyr Ala Ile  
155 160 165  
Gly Glu Lys Phe Ala Pro Gly Pro Ser Ala Cys Pro Cys Leu Cys  
170 175 180  
Thr Glu Glu Gly Pro Leu Cys Ala Gln Pro Glu Cys Pro Arg Leu  
185 190 195  
His Pro Arg Cys Ile His Val Asp Thr Ser Gln Cys Cys Pro Gln  
200 205 210  
Cys Lys Glu Arg Lys Asn Tyr Cys Glu Phe Arg Gly Lys Thr Tyr  
215 220 225  
Gln Thr Leu Glu Glu Phe Val Val Ser Pro Cys Glu Arg Cys Arg

	230	235	240
Cys Glu Ala Asn Gly Glu Val Leu Cys Thr Val Ser Ala Cys Pro			
245	250	255	
Gln Thr Glu Cys Val Asp Pro Val Tyr Glu Pro Asp Gln Cys Cys			
260	265	270	
Pro Ile Cys Lys Asn Gly Pro Asn Cys Phe Ala Glu Thr Ala Val			
275	280	285	
Ile Pro Ala Gly Arg Glu Val Lys Thr Asp Glu Cys Thr Ile Cys			
290	295	300	
His Cys Thr Tyr Glu Glu Gly Thr Trp Arg Ile Glu Arg Gln Ala			
305	310	315	
Met Cys Thr Arg His Glu Cys Arg Gln Met			
320	325		

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<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 12  
gaggtgtcgc tgtgaagcca acgg 24

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

<400> 13  
cgctcgattc tccatgtgcc ttcc 24

<210> 14  
<211> 45  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic Oligonucleotide Probe

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<210> 15  
<211> 1587  
<212> DNA  
<213> Homo sapiens

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gttcagcatg tgtggaaagg gtccgaccta ccccgaaat ggaccctaa 150  
gaacaccagc tgcgacagcg gcttgggtg ccaggacacg ttgatgtca 200  
ttgagagcgg accccaagtg agcctggcgc tctccaaggg ctgcacggag 250  
gccaaggacc aggagccccg cgtcaactgag cacccggatgg gccccggct 300  
ctccctgatc tcctacacct tcgtgtgccc ccaggaggac ttctgcaaca 350  
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ggatccttga ggtgcccagt ctgcttgcgt atgaaaggct gtctggaggg 450  
gacaacagaa gagatctgcc ccaagggac cacacactgt tatgatggcc 500  
tcctcaggct caggggagga ggcattttct ccaatctgag agtccaggga 550  
tgcatgcccc agccaggttg caacctgctc aatggacac agaaaattgg 600  
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tggtggggag tggtttggcc ttccctgctaa ctctattacc cccacgattc 1350  
ttcaccgctg ctgaccaccc acactcaacc tccctctgac ctcataaccc 1400  
aatggccttg gacaccagat tctttcccat tctgtccatg aatcatcttc 1450

cccacacaca atcattcata tctactcacc taacagcaac actggggaga 1500  
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 Leu Pro Gly Val Gln Ala Leu Leu Cys Gln Phe Gly Thr Val Gln  
     20             25                                 30  
  
 His Val Trp Lys Val Ser Asp Leu Pro Arg Gln Trp Thr Pro Lys  
     35             40                                45  
  
 Asn Thr Ser Cys Asp Ser Gly Leu Gly Cys Gln Asp Thr Leu Met  
     50             55                                60  
  
 Leu Ile Glu Ser Gly Pro Gln Val Ser Leu Val Leu Ser Lys Gly  
     65             70                                75  
  
 Cys Thr Glu Ala Lys Asp Gln Glu Pro Arg Val Thr Glu His Arg  
     80             85                                90  
  
 Met Gly Pro Gly Leu Ser Leu Ile Ser Tyr Thr Phe Val Cys Arg  
     95             100                             105  
  
 Gln Glu Asp Phe Cys Asn Asn Leu Val Asn Ser Leu Pro Leu Trp  
    110             115                             120  
  
 Ala Pro Gln Pro Pro Ala Asp Pro Gly Ser Leu Arg Cys Pro Val  
    125             130                             135  
  
 Cys Leu Ser Met Glu Gly Cys Leu Glu Gly Thr Thr Glu Glu Ile  
    140             145                             150  
  
 Cys Pro Lys Gly Thr Thr His Cys Tyr Asp Gly Leu Leu Arg Leu  
    155             160                             165  
  
 Arg Gly Gly Gly Ile Phe Ser Asn Leu Arg Val Gln Gly Cys Met  
    170             175                             180  
  
 Pro Gln Pro Gly Cys Asn Leu Leu Asn Gly Thr Gln Glu Ile Gly  
    185             190                             195  
  
 Pro Val Gly Met Thr Glu Asn Cys Asn Arg Lys Asp Phe Leu Thr  
    200             205                             210  
  
 Cys His Arg Gly Thr Thr Ile Met Thr His Gly Asn Leu Ala Gln  
    215             220                             225  
  
 Glu Pro Thr Asp Trp Thr Thr Ser Asn Thr Glu Met Cys Glu Val

230	235	240
Gly Gln Val Cys Gln Glu Thr Leu Leu Leu Ile Asp Val Gly Leu		
245	250	255
Thr Ser Thr Leu Val Gly Thr Lys Gly Cys Ser Thr Val Gly Ala		
260	265	270
Gln Asn Ser Gln Lys Thr Thr Ile His Ser Ala Pro Pro Gly Val		
275	280	285
Leu Val Ala Ser Tyr Thr His Phe Cys Ser Ser Asp Leu Cys Asn		
290	295	300
Ser Ala Ser Ser Ser Val Leu Leu Asn Ser Leu Pro Pro Gln		
305	310	315
Ala Ala Pro Val Pro Gly Asp Arg Gln Cys Pro Thr Cys Val Gln		
320	325	330
Pro Leu Gly Thr Cys Ser Ser Gly Ser Pro Arg Met Thr Cys Pro		
335	340	345
Arg Gly Ala Thr His Cys Tyr Asp Gly Tyr Ile His Leu Ser Gly		
350	355	360
Gly Gly Leu Ser Thr Lys Met Ser Ile Gln Gly Cys Val Ala Gln		
365	370	375
Pro Ser Ser Phe Leu Leu Asn His Thr Arg Gln Ile Gly Ile Phe		
380	385	390
Ser Ala Arg Glu Lys Arg Asp Val Gln Pro Pro Ala Ser Gln His		
395	400	405
Glu Gly Gly Ala Glu Gly Leu Glu Ser Leu Thr Trp Gly Val		
410	415	420
Gly Leu Ala Leu Ala Pro Ala Leu Trp Trp Gly Val Val Cys Pro		
425	430	435
Ser Cys		

<210> 17  
<211> 2387  
<212> DNA  
<213> Homo sapiens

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tcttagagccg agggaccggg tggcctcgcc gtcagcccc tatttcggca 150  
ccaagactcg ctacgaggat gtcaaccccg tgctattgtc gggccccgag 200

gctccgtggc gggaccctga gctgctggag gggacctgca ccccggtgca 250  
gctggtcgcc ctcattcgcc acggcacccg ctaccccacg gtcaaacaga 300  
tccgcaagct gaggcagctg cacgggttgc tgcagggccg cgggtccagg 350  
gatggcgggg ctagtagtac cggcagccgc gacctgggtg cagegctggc 400  
cgactggcct ttgtggtacg cggaactggat ggacgggcag ctagtagaga 450  
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gcagctactt tgcaagtgcc agtaaatgat taaaatgcag atttaattca 850  
atagccttt ttcacctgtt catttgacct ggcaattaaa ggtgttaat 900  
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ttaaatgatc tgaaacaata ttggaaaaga ggatatgggt atactattaa 1000  
cagtcgatcc agctgcaccc tggttcagga tatcttcag cacttggaca 1050  
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agtaacaaaa tatctcagtt ggaccatcct taacttgatt gaactgtcta 1850  
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atgtttggac aattagcaac aagtccgata gttagaatcg aagttttca 2200  
aatccattgc ttagcttaact ttttcattct gtcacttggc ttcatgtttt 2250  
atattttcctt attatatgaa atgtatcttt tggttgtttt atttttcttt 2300  
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ctataataaa gaaaattctt gtgactttaa aaaaaaaaa 2387

<210> 18  
<211> 487  
<212> PRT  
<213> Homo sapiens

<400> 18  
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20 25 30  
Ser Leu Leu Glu Pro Arg Asp Pro Val Ala Ser Ser Leu Ser Pro  
35 40 45  
Tyr Phe Gly Thr Lys Thr Arg Tyr Glu Asp Val Asn Pro Val Leu  
50 55 60  
Leu Ser Gly Pro Glu Ala Pro Trp Arg Asp Pro Glu Leu Leu Glu  
65 70 75  
Gly Thr Cys Thr Pro Val Gln Leu Val Ala Leu Ile Arg His Gly  
80 85 90  
Thr Arg Tyr Pro Thr Val Lys Gln Ile Arg Lys Leu Arg Gln Leu  
95 100 105  
His Gly Leu Leu Gln Ala Arg Gly Ser Arg Asp Gly Ala Ser

	110	115	120
Ser Thr Gly Ser Arg Asp Leu Gly Ala Ala Leu Ala Asp Trp Pro			
125	130	135	
Leu Trp Tyr Ala Asp Trp Met Asp Gly Gln Leu Val Glu Lys Gly			
140	145	150	
Arg Gln Asp Met Arg Gln Leu Ala Leu Arg Leu Ala Ser Leu Phe			
155	160	165	
Pro Ala Leu Phe Ser Arg Glu Asn Tyr Gly Arg Leu Arg Leu Ile			
170	175	180	
Thr Ser Ser Lys His Arg Cys Met Asp Ser Ser Ala Ala Phe Leu			
185	190	195	
Gln Gly Leu Trp Gln His Tyr His Pro Gly Leu Pro Pro Pro Asp			
200	205	210	
Val Ala Asp Met Glu Phe Gly Pro Pro Thr Val Asn Asp Lys Leu			
215	220	225	
Met Arg Phe Phe Asp His Cys Glu Lys Phe Leu Thr Glu Val Glu			
230	235	240	
Lys Asn Ala Thr Ala Leu Tyr His Val Glu Ala Phe Lys Thr Gly			
245	250	255	
Pro Glu Met Gln Asn Ile Leu Lys Lys Val Ala Ala Thr Leu Gln			
260	265	270	
Val Pro Val Asn Asp Leu Asn Ala Asp Leu Ile Gln Val Ala Phe			
275	280	285	
Phe Thr Cys Ser Phe Asp Leu Ala Ile Lys Gly Val Lys Ser Pro			
290	295	300	
Trp Cys Asp Val Phe Asp Ile Asp Asp Ala Lys Val Leu Glu Tyr			
305	310	315	
Leu Asn Asp Leu Lys Gln Tyr Trp Lys Arg Gly Tyr Gly Tyr Thr			
320	325	330	
Ile Asn Ser Arg Ser Ser Cys Thr Leu Phe Gln Asp Ile Phe Gln			
335	340	345	
His Leu Asp Lys Ala Val Glu Gln Lys Gln Arg Ser Gln Pro Ile			
350	355	360	
Ser Ser Pro Val Ile Leu Gln Phe Gly His Ala Glu Thr Leu Leu			
365	370	375	
Pro Leu Leu Ser Leu Met Gly Tyr Phe Lys Asp Lys Glu Pro Leu			
380	385	390	
Thr Ala Tyr Asn Tyr Lys Lys Gln Met His Arg Lys Phe Arg Ser			
395	400	405	

Gly Leu Ile Val Pro Tyr Ala Ser Asn Leu Ile Phe Val Leu Tyr  
410 415 420

His Cys Glu Asn Ala Lys Thr Pro Lys Glu Gln Phe Arg Val Gln  
425 430 435

Met Leu Leu Asn Glu Lys Val Leu Pro Leu Ala Tyr Ser Gln Glu  
440 445 450

Thr Val Ser Phe Tyr Glu Asp Leu Lys Asn His Tyr Lys Asp Ile  
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Leu Gln Ser Cys Gln Thr Ser Glu Glu Cys Glu Leu Ala Arg Ala  
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Asn Ser Thr Ser Asp Glu Leu  
485

<210> 19  
<211> 3554  
<212> DNA  
<213> Homo sapiens

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cttcttcctg ctgtgtcttt tcagggctg cctgataagg gctgtaaaatc 150  
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cgttgtcgaa aatgaccgca agggaaatttga tgagattgtg atcgagttaa 450  
ctgtgcaagt gaagccagtg acccctgtct gttagagtgcg gaaggctgta 500  
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gttgtccttg ctgtactggc cctgatcagc ttgggcacgt gctgtgcata 850

cagacgtggc tacttcatca acaataaaaca ggatggagaa agttacaaga 900  
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tattttgatt attgaaaaga aaatttctat tttaactgta aatatattgt 1800  
catacaatgt taaataaacct attttttaa aaaagttcaa cttaaggtag 1850  
aagttccaag ctactagtgt taaattggaa aatataataa attaagagta 1900  
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cacacaagtt ttagcccttt tcacaaggaa actcatactg tctacacatc 2000  
agaccatagt tgcttagaa acctttaaaa attccagttt agcaatgttg 2050  
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gcctcttctt gagatgacta ggacagtctg tacccagagg ccacccagaa 2150  
gccctcagat gtacatacac agatgccagt cagctccctgg gggtgcgc 2200  
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aaagaacgtc aggtggagca gccaggtgaa aggccctggcg gggaggaaag 2700  
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aagatatgaa tgtgactcaa gactcgaggg cgatacgagg ctgtgattct 3450  
gcctttggat ggatgttgct gtacacagat gctacagact tgtactaaca 3500  
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ccca 3554

<210> 20  
<211> 310  
<212> PRT  
<213> Homo sapiens

<400> 20

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					20			25					30	
Ala	Val	Asn	Leu	Lys	Ser	Ser	Asn	Arg	Thr	Pro	Val	Val	Gln	Glu
					35			40					45	
Phe	Glu	Ser	Val	Glu	Leu	Ser	Cys	Ile	Ile	Thr	Asp	Ser	Gln	Thr
					50			55					60	
Ser	Asp	Pro	Arg	Ile	Glu	Trp	Lys	Ile	Gln	Asp	Glu	Gln	Thr	
					65			70					75	
Thr	Tyr	Val	Phe	Phe	Asp	Asn	Lys	Ile	Gln	Gly	Asp	Leu	Ala	Gly
					80			85					90	
Arg	Ala	Glu	Ile	Leu	Gly	Lys	Thr	Ser	Leu	Lys	Ile	Trp	Asn	Val
					95			100					105	
Thr	Arg	Arg	Asp	Ser	Ala	Leu	Tyr	Arg	Cys	Glu	Val	Val	Ala	Arg
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Asn	Asp	Arg	Lys	Glu	Ile	Asp	Glu	Ile	Val	Ile	Glu	Leu	Thr	Val
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Gln	Val	Lys	Pro	Val	Thr	Pro	Val	Cys	Arg	Val	Pro	Lys	Ala	Val
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His	Pro	Arg	Pro	His	Tyr	Ser	Trp	Tyr	Arg	Asn	Asp	Val	Pro	Leu
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Pro	Thr	Asp	Ser	Arg	Ala	Asn	Pro	Arg	Phe	Arg	Asn	Ser	Ser	Phe
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His	Leu	Asn	Ser	Glu	Thr	Gly	Thr	Leu	Val	Phe	Thr	Ala	Val	His
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Lys	Asp	Asp	Ser	Gly	Gln	Tyr	Tyr	Cys	Ile	Ala	Ser	Asn	Asp	Ala
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Gly	Ser	Ala	Arg	Cys	Glu	Glu	Gln	Glu	Met	Glu	Val	Tyr	Asp	Leu
					230			235					240	
Asn	Ile	Gly	Gly	Ile	Ile	Gly	Gly	Val	Leu	Val	Val	Leu	Ala	Val
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Leu	Ala	Leu	Ile	Thr	Leu	Gly	Ile	Cys	Cys	Ala	Tyr	Arg	Arg	Gly
					260			265					270	
Tyr	Phe	Ile	Asn	Asn	Lys	Gln	Asp	Gly	Glu	Ser	Tyr	Lys	Asn	Pro
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Gly	Lys	Pro	Asp	Gly	Val	Asn	Tyr	Ile	Arg	Thr	Asp	Glu	Glu	Gly

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<211> 3437

<212> DNA

<213> Homo sapiens

<400> 21

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gagccgacga cagcgagtcc caggcgctgc tggacatctg gtttccggag 150  
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<211> 1029

<212> PRT

<213> Homo sapiens

<400> 22

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					20				25				30	

Ile	Trp	Phe	Pro	Glu	Glu	Lys	Pro	Leu	Pro	Thr	Ala	Phe	Leu	Val
				35					40			45		

Asp	Thr	Ser	Glu	Glu	Ala	Leu	Leu	Leu	Pro	Asp	Trp	Leu	Lys	Leu
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Arg	Met	Ile	Arg	Ser	Glu	Val	Leu	Arg	Leu	Val	Asp	Ala	Ala	Leu
					65				70			75		

Gln	Asp	Leu	Glu	Pro	Gln	Gln	Leu	Leu	Leu	Phe	Val	Gln	Ser	Phe
					80				85			90		

Gly	Ile	Pro	Val	Ser	Ser	Met	Ser	Lys	Leu	Leu	Gln	Phe	Leu	Asp
					95				100			105		

Gln Ala Val Ala His Asp Pro Gln Thr Leu Glu Gln Asn Ile Met  
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 Asp Lys Asn Tyr Met Ala His Leu Val Glu Val Gln His Glu Arg  
 125 130 135  
 Gly Ala Ser Gly Gly Gln Thr Phe His Ser Leu Leu Thr Ala Ser  
 140 145 150  
 Leu Pro Pro Arg Arg Asp Ser Thr Glu Ala Pro Lys Pro Lys Ser  
 155 160 165  
 Ser Pro Glu Gln Pro Ile Gly Gln Gly Arg Ile Arg Val Gly Thr  
 170 175 180  
 Gln Leu Arg Val Leu Gly Pro Glu Asp Asp Leu Ala Gly Met Phe  
 185 190 195  
 Leu Gln Ile Phe Pro Leu Ser Pro Asp Pro Arg Trp Gln Ser Ser  
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 Ser Pro Arg Pro Val Ala Leu Ala Leu Gln Gln Ala Leu Gly Gln  
 215 220 225  
 Glu Leu Ala Arg Val Val Gln Gly Ser Pro Glu Val Pro Gly Ile  
 230 235 240  
 Thr Val Arg Val Leu Gln Ala Leu Ala Thr Leu Leu Ser Ser Pro  
 245 250 255  
 His Gly Gly Ala Leu Val Met Ser Met His Arg Ser His Phe Leu  
 260 265 270  
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 Pro Gln Asp Thr Gly Phe Ser Ser Leu Phe Leu Lys Val Leu Leu  
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 320 325 330  
 Arg Arg Leu Ser Asp Val Arg Gly Gly Leu Leu Arg Leu Ala Glu  
 335 340 345  
 Ala Leu Ala Phe Arg Gln Asp Leu Glu Val Val Ser Ser Thr Val  
 350 355 360  
 Arg Ala Val Ile Ala Thr Leu Arg Ser Gly Glu Gln Cys Ser Val  
 365 370 375  
 Glu Pro Asp Leu Ile Ser Lys Val Leu Gln Gly Leu Ile Glu Val  
 380 385 390  
 Arg Ser Pro His Leu Glu Glu Leu Leu Thr Ala Phe Phe Ser Ala

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Gly Lys Pro Gly Ala Asp Gly Gly Ser Leu Glu Ala Val Arg Leu		
440	445	450
Gly Pro Ser Ser Gly Leu Leu Val Asp Trp Leu Glu Met Leu Asp		
455	460	465
Pro Glu Val Val Ser Ser Cys Pro Asp Leu Gln Leu Arg Leu Leu		
470	475	480
Phe Ser Arg Arg Lys Gly Lys Gly Gln Ala Gln Val Pro Ser Phe		
485	490	495
Arg Pro Tyr Leu Leu Thr Leu Phe Thr His Gln Ser Ser Trp Pro		
500	505	510
Thr Leu His Gln Cys Ile Arg Val Leu Leu Gly Lys Ser Arg Glu		
515	520	525
Gln Arg Phe Asp Pro Ser Ala Ser Leu Asp Phe Leu Trp Ala Cys		
530	535	540
Ile His Val Pro Arg Ile Trp Gln Gly Arg Asp Gln Arg Thr Pro		
545	550	555
Gln Lys Arg Arg Glu Glu Leu Val Leu Arg Val Gln Gly Pro Glu		
560	565	570
Leu Ile Ser Leu Val Glu Leu Ile Leu Ala Glu Ala Glu Thr Arg		
575	580	585
Ser Gln Asp Gly Asp Thr Ala Ala Cys Ser Leu Ile Gln Ala Arg		
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Leu Pro Leu Leu Leu Ser Cys Cys Gly Asp Asp Glu Ser Val		
605	610	615
Arg Lys Val Thr Glu His Leu Ser Gly Cys Ile Gln Gln Trp Gly		
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Asp Ser Val Leu Gly Arg Arg Cys Arg Asp Leu Leu Leu Gln Leu		
635	640	645
Tyr Leu Gln Arg Pro Glu Leu Arg Val Pro Val Pro Glu Val Leu		
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Leu His Ser Glu Gly Ala Ala Ser Ser Val Cys Lys Leu Asp		
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Gly Leu Ile His Arg Phe Ile Thr Leu Leu Ala Asp Thr Ser Asp		
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 Arg Lys Leu<sup>\*</sup> Ala Val Ala His Pro Leu Leu Leu Leu Arg His Leu  
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 Pro Met Ile Ala Ala Leu Leu His Gly Arg Thr His Leu Asn Phe  
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 Gln Glu Phe Arg Gln Gln Asn His Leu Ser Cys Phe Leu His Val  
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 Leu Gly Leu Leu Glu Leu Leu Gln Pro His Val Phe Arg Ser Glu  
 755 760 765  
 His Gln Gly Ala Leu Trp Asp Cys Leu Leu Ser Phe Ile Arg Leu  
 770 775 780  
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 Asn Lys Phe Val Gln Phe Ile His Lys Tyr Ile Thr Tyr Asn Ala  
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 Pro Ala Ala Ile Ser Phe Leu Gln Lys His Ala Asp Pro Leu His  
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 Asp Leu Ser Phe Asp Asn Ser Asp Leu Val Met Leu Lys Ser Leu  
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 Leu Ala Gly Leu Ser Leu Pro Ser Arg Asp Asp Arg Thr Asp Arg  
 845 850 855  
 Gly Leu Asp Glu Glu Gly Glu Glu Ser Ser Ala Gly Ser Leu  
 860 865 870  
 Pro Leu Val Ser Val Ser Leu Phe Thr Pro Leu Thr Ala Ala Glu  
 875 880 885  
 Met Ala Pro Tyr Met Lys Arg Leu Ser Arg Gly Gln Thr Val Glu  
 890 895 900  
 Asp Leu Leu Glu Val Leu Ser Asp Ile Asp Glu Met Ser Arg Arg  
 905 910 915  
 Arg Pro Glu Ile Leu Ser Phe Phe Ser Thr Asn Leu Gln Arg Leu  
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 Met Ser Ser Ala Glu Glu Cys Cys Arg Asn Leu Ala Phe Ser Leu  
 935 940 945  
 Ala Leu Arg Ser Met Gln Asn Ser Pro Ser Ile Ala Ala Ala Phe  
 950 955 960  
 Leu Pro Thr Phe Met Tyr Cys Leu Gly Ser Gln Asp Phe Glu Val  
 965 970 975  
 Val Gln Thr Ala Leu Arg Asn Leu Pro Glu Tyr Ala Leu Leu Cys

980	985	990
Gln Glu His Ala Ala Val Leu Leu His Arg Ala Phe Leu Val Gly		
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Arg Ile Leu His Met Glu Ala Val Met		
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<212> DNA  
<213> Homo sapiens

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Gln Lys Gly Asp Val Val Asp Val Tyr Gln Arg Glu Phe Leu Ala  
35 40 45

Leu Arg Asp Arg Leu His Ala Ala Glu Gln Glu Ser Leu Lys Arg  
50 55 60

Ser Lys Glu Leu Asn Leu Val Leu Asp Glu Ile Lys Arg Ala Val  
65 70 75

Ser Glu Arg Gln Ala Leu Arg Asp Gly Asp Gly Asn Arg Thr Trp  
80 85 90

Gly Arg Leu Thr Glu Asp Pro Arg Leu Lys Pro Trp Asn Gly Ser  
95 100 105

His Arg His Val Leu His Leu Pro Thr Val Phe His His Leu Pro  
110 115 120

His Leu Leu Ala Lys Glu Ser Ser Leu Gln Pro Ala Val Arg Val  
125 130 135

Gly Gln Gly Arg Thr Gly Val Ser Val Val Met Gly Ile Pro Ser  
140 145 150

Val Arg Arg Glu Val His Ser Tyr Leu Thr Asp Thr Leu His Ser  
155 160 165

Leu Ile Ser Glu Leu Ser Pro Gln Glu Lys Glu Asp Ser Val Ile  
170 175 180

Val Val Leu Ile Ala Glu Thr Asp Ser Gln Tyr Thr Ser Ala Val  
185 190 195

Thr Glu Asn Ile Lys Ala Leu Phe Pro Thr Glu Ile His Ser Gly  
200 205 210

Leu Leu Glu Val Ile Ser Pro Ser Pro His Phe Tyr Pro Asp Phe  
215 220 225

Ser Arg Leu Arg Glu Ser Phe Gly Asp Pro Lys Glu Arg Val Arg  
230 235 240

Trp Arg Thr Lys Gln Asn Leu Asp Tyr Cys Phe Leu Met Met Tyr  
245 250 255

Ala Gln Ser Lys Gly Ile Tyr Tyr Val Gln Leu Glu Asp Asp Ile  
260 265 270

Val Ala Lys Pro Asn Tyr Leu Ser Thr Met Lys Asn Phe Ala Leu  
275 280 285

Gln Gln Pro Ser Glu Asp Trp Met Ile Leu Glu Phe Ser Gln Leu  
290 295 300

Gly Phe Ile Gly Lys Met Phe Lys Ser Leu Asp Leu Ser Leu Ile  
305 310 315

Val Glu Phe Ile Leu Met Phe Tyr Arg Asp Lys Pro Ile Asp Trp

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Asp Ala Lys His Cys Asp Arg Gln Lys Ala Asn Leu Arg Ile Arg		
350	355	360
Phe Lys Pro Ser Leu Phe Gln His Val Gly Thr His Ser Ser Leu		
365	370	375
Ala Gly Lys Ile Gln Lys Leu Lys Asp Lys Asp Phe Gly Lys Gln		
380	385	390
Ala Leu Arg Lys Glu His Val Asn Pro Pro Ala Glu Val Ser Thr		
395	400	405
Ser Leu Lys Thr Tyr Gln His Phe Thr Leu Glu Lys Ala Tyr Leu		
410	415	420
Arg Glu Asp Phe Phe Trp Ala Phe Thr Pro Ala Ala Gly Asp Phe		
425	430	435
Ile Arg Phe Arg Phe Phe Gln Pro Leu Arg Leu Glu Arg Phe Phe		
440	445	450
Phe Arg Ser Gly Asn Ile Glu His Pro Glu Asp Lys Leu Phe Asn		
455	460	465
Thr Ser Val Glu Val Leu Pro Phe Asp Asn Pro Gln Ser Asp Lys		
470	475	480
Glu Ala Leu Gln Glu Gly Arg Thr Ala Thr Leu Arg Tyr Pro Arg		
485	490	495
Ser Pro Asp Gly Tyr Leu Gln Ile Gly Ser Phe Tyr Lys Gly Val		
500	505	510
Ala Glu Gly Glu Val Asp Pro Ala Phe Gly Pro Leu Glu Ala Leu		
515	520	525
Arg Leu Ser Ile Gln Thr Asp Ser Pro Val Trp Val Ile Leu Ser		
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<400> 31  
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<210> 34  
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<223> Synthetic Oligonucleotide Probe

<400> 34  
cttctgggcc acagccctgc 20

<210> 35  
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